BIOTECHNOLOGY
SYSTEMS
BRANCH

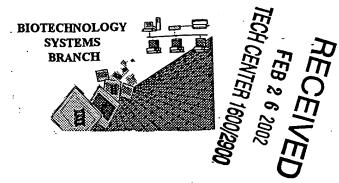# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/483,837A_

Source: _1600_

Date Processed by STIC: _2/12/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
    APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
    NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
    Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
    2011 South Clark Place, Arlington, VA 22202
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   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/483,837A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

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1600

RAW SEQUENCE LISTING   DATE: 02/12/2002
PATENT APPLICATION: US/09/483,837A   TIME: 13:19:43

Input Set : A:\EP.txt
Output Set: N:\CRF3\02122002\I483837A.raw

Does Not Comply Corrected Diskette Needed

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  3 <110> APPLICANT: Palatin Technologies, Inc.
  4        Sharma, Shubh
  6 <120> TITLE OF INVENTION: Metallopeptide and Metalloconstruct Combinatorial Libraries
and
  7        Applications
  9 <130> FILE REFERENCE: 70025-9902-11
 11 <140> CURRENT APPLICATION NUMBER: US 09/483,837A
 12 <141> CURRENT FILING DATE: 2000-01-17
 14 <150> PRIOR APPLICATION NUMBER: US 08/660,697
 15 <151> PRIOR FILING DATE: 1996-06-06
 17 <150> PRIOR APPLICATION NUMBER: US 08/476,652
 18 <151> PRIOR FILING DATE: 1995-06-07
 20 <150> PRIOR APPLICATION NUMBER: US 09/464,358
 21 <151> PRIOR FILING DATE: 1999-12-15
 23 <160> NUMBER OF SEQ ID NOS: 10
 25 <170> SOFTWARE: PatentIn version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 4
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Artificial
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: peptide
 35 <220> FEATURE:
 36 <221> NAME/KEY: MOD_RES
 37 <222> LOCATION: (4)..(4)
 38 <223> OTHER INFORMATION: Xaa is bAla
 41 <400> SEQUENCE: 1
 43 Arg Gly Cys Xaa
 44 1
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 4
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Artificial
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: peptide
 54 <220> FEATURE:
 55 <221> NAME/KEY: misc_feature
 56 <223> OTHER INFORMATION: Xaa is bAla
 59 <400> SEQUENCE: 2
 61 Gly Arg Cys Xaa
 62 1
 64 <210> SEQ ID NO: 3
 65 <211> LENGTH: 4
 66 <212> TYPE: PRT
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(handwritten annotations) insufficient explanation — see item 11 on Error Summary Sheet

(handwritten) same error → <222> (4)..(4) ← insert

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/483,837A

DATE: 02/12/2002
TIME: 13:19:43

Input Set : A:\EP.txt
Output Set: N:\CRF3\02122002\I483837A.raw

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     70 <223> OTHER INFORMATION: (peptide)
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     75 1
     77 <210> SEQ ID NO: 4
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C--> 80 <213> ORGANISM: Artificial
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     88 1
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     92 <212> TYPE: PRT
C--> 93 <213> ORGANISM: Artificial
     95 <220> FEATURE:
     96 <223> OTHER INFORMATION: (peptide)
     98 <400> SEQUENCE: 5
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    101 1                   5
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    104 <211> LENGTH: 6
    105 <212> TYPE: PRT
C--> 106 <213> ORGANISM: Artificial
    108 <220> FEATURE:
    109 <223> OTHER INFORMATION: synthetic peptide metallothionein sequence
    111 <400> SEQUENCE: 6
    113 Lys Cys Thr Cys Cys Ala
    114 1               5
    116 <210> SEQ ID NO: 7
    117 <211> LENGTH: 5
    118 <212> TYPE: PRT
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    121 <220> FEATURE:
    122 <223> OTHER INFORMATION: laminin sequence
    124 <400> SEQUENCE: 7
    126 Tyr Ile Gly Ser Arg
    127 1               5
    129 <210> SEQ ID NO: 8
    130 <211> LENGTH: 6
    131 <212> TYPE: PRT
C--> 132 <213> ORGANISM: Artificial
    134 <220> FEATURE:
    135 <223> OTHER INFORMATION: laminin sequence
    137 <400> SEQUENCE: 8
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      140 1               5
      142 <210> SEQ ID NO: 9
      143 <211> LENGTH: 4
      144 <212> TYPE: PRT
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      147 <220> FEATURE:
      148 <223> OTHER INFORMATION: peptide
      150 <400> SEQUENCE: 9
      152 Phe Gly Cys Arg
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      155 <210> SEQ ID NO: 10
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      157 <212> TYPE: PRT
C-->  158 <213> ORGANISM: Artificial
      160 <220> FEATURE:
      161 <223> OTHER INFORMATION: peptide
      163 <400> SEQUENCE: 10
      165 Gly Gly Gly Gly
      166 1
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VERIFICATION SUMMARY   DATE: 02/12/2002
PATENT APPLICATION: US/09/483,837A   TIME: 13:19:44

Input Set : A:\EP.txt
Output Set: N:\CRF3\02122002\I483837A.raw

L:30 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:49 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:61 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:67 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:80 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:93 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:106 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:119 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:132 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:145 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:158 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10